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Confirmation of*Naja oxiana* in Himachal Pradesh, India.

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The Central Asian Cobra *Naja oxiana* (Eichwald, 1831), also called the Caspian, Oxus, or Russian cobra, is a species of venomous snake in the family Elapidae. *Naja oxiana* exhibits considerable ontogenetic variation in its pattern, however juveniles tend to be pale, with a faded appearance. Juveniles additionally have noticeable dark and light cross-bands of approximately equal width around the body. Adults are completely light to chocolate brown or yellowish, with some specimens retaining traces of juvenile banding, especially the first few dark ventral bands (Wüster, 1998).

Naja oxiana was originally considered a subspecies of the Indian, spectacled, Asian or binocellate cobra *Naja naja* (Wüster & Thorpe, 1992) and little was known about its distribution in India (Mahajan & Agrawal, 1976). Whilst *N. naja* is confidently recorded throughout the majority of India, with the exception of the northeastern states, the distribution of *N. oxiana* is still in need of confirmation (Whitaker & Captain, 2008).The older literature frequently used the names *Naja n. oxiana* or *N. naja* for several species of Asiatic cobras prior to their reclassification (Wüster, 1998), and reported the distribution of *N. oxiana*as including north-west India, but with no specific locations (Biswas & Sanyal, 1977). The frequent absence of hood marks in many *Naja naja* from northern India often led to these specimens being misidentified as *N. oxiana*, further adding to the confusion (Wüster, 1998). In Wüster & Thorpe's (1992) review of published records of *N. oxiana* from northern India, the only records considered reliable were from Jammu (Murthy & Sharma, 1976; Murthy *et al*., 1979), and from Solan District, Himachal Pradesh (Mahajan & Agrawal, 1976). Reports from elsewhere in India appear to be due to misidentification of the melanistic morph of *N. naja*, which lacks an obvious spectacle hood mark (Saika *et al*., 2007). The status of the species in India has been all the more mysterious since there have been no confirmed records from India since the 1970s.

Here, we report new observations of *N. oxiana* (Figure 1) from Himachal Pradesh in 2017 and 2018. Two live *N. oxiana* specimens were encountered in the area surrounding Majoga, in the district of Chamba (see Figure 2), during a research expedition undertaken as part of the Bangor University Biodiversity Informatics and Technology Exchange for the Management of Snakebite (BITES) project in 2017. Two further *N. oxiana* specimens were encountered between June and September 2018 during a collaborative research expedition by the BITES, Simultala Conservationists (Foundation for Wildlife) and Captive & Field Herpetology teams. All individuals were found on grassy / rocky slopes with sparse mixed alpine shrub and tree cover with occasional large rocks, boulders and rock faces,

or on agricultural land and pasture. Occurring on typically low inclines, individuals were found in microhabitats with a dense cover of *Cannabis*.

Figure 1 location

Figure 2 location

Identification was confirmed using characters from Wüster (1998) and phylogenetic analysis. Morphological characteristics are provided in Table 1. Interestingly, the ventral and subcaudal scale counts of the new Himachal Pradesh specimens are slightly below the range previously reported (Wüster, 1998), and within the range of corresponding counts in *N. naja*, but the low dorsal scale row counts around the neck and the pattern are characteristic of *N. oxiana.*

Table 1: Sample data and morphological characteristics of *Naja oxiana* in Himachal Pradesh, India.

Species	*Naja oxiana*	*Naja oxiana*	*Naja oxiana*	*Naja oxiana*
Reference Number	17.V18	17.V19	18.16	18.51
Date	21.09.2017	22.09.2017	11.07.2018	16.08.2018
Time (h GMT+5.5 h)	Not recorded	Not recorded	21:56	22:13
Elevation (m a.s.l.)	1900	2100	2021	1565
Morphology				
Sex	Female	Female	Female	Female
Snout-Vent Length (cm)	99	98	91	106
Tail Length (cm)	14	18.5	18.3	21.5
Visible neck banding	Present	Absent	Present	Absent
Hood markings	Present	Absent	Present	Absent
Cuneate scale	Absent (The left 3rd and 4th infralabial scales were damaged)	1 cuneate scale on the left side between 3rd and 4th infralabials	1 cuneate scale between 3rd and 4th infralabial on both sides	-
Scalation				
Scale rows at mid-body	21	21	21	21
Scale rows round neck	23	23	23	22
Scale rows before vent (one head length ahead of vent)	16	15	15	15
Ventrals*	189	190	189	189
Subcaudals (all paired)	37 (Tail tip missing)	57	60	61

First V of first dark band (ventral scale no.)	6th	6th	6th	5th
Last V of first dark band (ventral scale no.)	8th	9th	9th	8th

*Recorded using the Dowling method (Dowling, 1950)

For 2017 samples, the evolutionary history was inferred using the Maximum Likelihood method based on the Tamura 3-parameter model (Tamura, 1992) in MEGA7 (Kumar, 2016). The analysis involved 20 nucleotide sequences comprising 421 base pairs of 16S large subunit ribosomal DNA, including three sequences of *N. oxiana* and one of *N. naja* generated specifically for this study. Other sequences were downloaded from GenBank. All positions with less than 90% site coverage were eliminated. The tree with the highest log likelihood (-1114.13) is shown in Figure 3. (only when >50%). A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories, parameter = 0.1132).

Figure 3 location

These observations confirm the continued presence of *N. oxiana* in northern India, and represent a species range extension of approximately 120 km east-north-east and 220 km north-west from the previous Indian records at Jammu and Solan District in Himachal Pradesh, respectively, and an elevation increase of 100m from 2000 m a.s.l. (Wüster, 1998) to 2100 m a.s.l.

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FIGURE LEGENDS

Figure 1: Female *Naja oxiana* displaying juvenile hood markings.

Figure 2: *Naja oxiana* location map.

Figure 3. *Naja oxiana* molecular phylogenetic analysis by Maximum Likelihood method. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Tips are labelled with associated Genbank Accession numbers. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.